<first sequence: ss.AR350065 (length = 1381)
<second sequence: ss.DNA57033 (length = 2056)

<1362 matches in an overlap of 1381: 98.62 percent similarity
<gaps in first sequence: 2 (3 bases), gaps in second sequence: 3 (3 bases)
<score: 4040 (match = 3, mismatch = 0, gap penalty = 8 + 1 per base)
<endgaps not penalized

GenBank (Release 143, aug 2004)[Sep 10 16:50:21 2004]:

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AR350065      Sequence 1 from patent US 6586228. 1381 bp,
              DNA, linear, PAT 17-AUG-2003
ACCESSION     AR350065
VERSION       AR350065.1  GI:33751016
KEYWORDS      .
SOURCE        Unknown.
  ORGANISM    Unknown.
              Unclassified.
REFERENCE   1   (bases 1 to 1381)
  AUTHORS     Parham,C.L., Moore,K.W. and Murgolo,N.J.
  TITLE       Polynucleotides encoding DIRS1
  JOURNAL     Patent: US 6586228-A 1 01-JUL-2003;
FEATURES                Location/Qualifiers
     source             1..1381
                        /organism="unknown"
                        /mol_type="genomic DNA."
BASE COUNT
ORIGIN
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ss.AR350065                                                               TCG
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ss.DNA57033   TGGGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAG
                     70        80        90       100       110       120

                     10        20        30        40        50        60
ss.AR350065   ACCCACGC-GTCCGCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAG
              *  *  *    *  *  *  *********************************************
ss.DNA57033   AACAATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAG
                    130       140       150       160       170       180

                     70        80        90       100       110       120
ss.AR350065   ATGGCTGAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACTGA
              ************************************************************
ss.DNA57033   ATGGCTGAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACTGA
                    190       200       210       220       230       240

                    130       140       150       160       170       180
ss.AR350065   GTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATG
              ************************************************************
ss.DNA57033   GTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATG
                    250       260       270       280       290       300
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                    190       200       210       220       230       240
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              ************************************************************
ss.DNA57033   TGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCC
                    310       320       330       340       350       360


                    250       260       270       280       290       300
ss.AR350065   CCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTG
              ************************************************************
ss.DNA57033   CCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTG
                    370       380       390       400       410       420


                    310       320       330       340       350       360
ss.AR350065   ATCGCGCCTGGAGAAACAGTGTACTATTCTGTCGAATACCAGGGGGAGTACGAGAGCCTG
              ************************************************************
ss.DNA57033   ATCGCGCCTGGAGAAACAGTGTACTATTCTGTCGAATACCAGGGGGAGTACGAGAGCCTG
                    430       440       450       460       470       480


                    370       380       390       400       410       420
ss.AR350065   TACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGT
              ************************************************************
ss.DNA57033   TACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGT
                    490       500       510       520       530       540


                    430       440       450       460       470       480
ss.AR350065   GATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTG
              ************************************************************
ss.DNA57033   GATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTG
                    550       560       570       580       590       600


                    490       500       510       520       530       540
ss.AR350065   GGCTCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATC
              ************************************************************
ss.DNA57033   GGCTCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATC
                    610       620       630       640       650       660


                    550       560       570       580       590       600
ss.AR350065   CTTACCCGACCTGGGATGGAGATCXCCAAAXATGGCTTCCACCTGGTTATTGAGCTGGAG
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ss.DNA57033   CTTACCCGACCTGGGATGGAGATCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAG
                    670       680       690       700       710       720


                    610       620       630       640       650       660
ss.AR350065   GACCTGGGGCCCCAGTTTGAGTTCCTTGTGGCCTACTGGASGAGGGAGCCTGGTGCCGAG
              ********************************* **************************
ss.DNA57033   GACCTGGGGCCCCAGTTTGAGTTCCTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAG
                    730       740       750       760       770       780


                    670       680       690       700       710       720
ss.AR350065   GAACATGTCAAAATGGTGAGGAGTGGGGGTATTCCAGTGCACCTAGAAACCATGGAGCCA
              ************************************************************
ss.DNA57033   GAACATGTCAAAATGGTGAGGAGTGGGGGTATTCCAGTGCACCTAGAAACCATGGAGCCA
                    790       800       810       820       830       840


                    730       740       750       760       770       780
ss.AR350065   GGGGCTGCATACTGTGTGAAGGCCCAGACATTCGTGAAGGCCATTGGGARGTACAGCGCC
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ss.DNA57033      GGGGCTGCATACTGTGTGAAGGCCCAGACATTCGTGAAGGCCATTGGGAGGTACAGCGCC
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                      790       800       810       820       830       840
ss.AR350065      TTCAGCCAGACAGAATGTGTGGARGTGCAAGGAGAGGCCATTCCCCTGGTACTGGCCCTG
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ss.DNA57033      TTCAGCCAGACAGAATGTGTGGAGGTGCAAGGAGAGGCCATTCCCCTGGTACTGGCCCTG
                      910       920       930       940       950       960


                      850       860       870       880       890       900
ss.AR350065      TTTGCCTTTGTTGGCTTCATGCTGATCCTTGTGGTCGTGCCACTGTTCGTCTGGAAAATG
                 ************************************************************
ss.DNA57033      TTTGCCTTTGTTGGCTTCATGCTGATCCTTGTGGTCGTGCCACTGTTCGTCTGGAAAATG
                      970       980       990      1000      1010      1020


                      910       920       930       940       950       960
ss.AR350065      GGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGGTGGTCCTCCCAGACACCTTGAAAATA
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ss.DNA57033      GGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGGTGGTCCTCCCAGACACCTTGAAAATA
                     1030      1040      1050      1060      1070      1080


                      970       980       990      1000      1010      1020
ss.AR350065      ACCAATTCACCCCAGAAGTTAATCAGCTGCAGAAGGGAGGAGGTGGATGCCTGTGCCACG
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ss.DNA57033      ACCAATTCACCCCAGAAGTTAATCAGCTGCAGAAGGGAGGAGGTGGATGCCTGTGCCACG
                     1090      1100      1110      1120      1130      1140


                     1030      1040      1050      1060      1070      1080
ss.AR350065      GCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGATCTCATAGGTTTGCGGAAGGGCC
                 ************************************************************
ss.DNA57033      GCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGATCTCATAGGTTTGCGGAAGGGCC
                     1150      1160      1170      1180      1190      1200


                     1090      1100      1110      1120      1130      1140
ss.AR350065      CAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACCATGAGGGGACAAGTTGTGTT
                 ************************************************************
ss.DNA57033      CAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACCATGAGGGGACAAGTTGTGTT
                     1210      1220      1230      1240      1250      1260


                     1150      1160      1170      1180      1190      1200
ss.AR350065      TCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGAGCCTGTTGTCTACAAGTC
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ss.DNA57033      TCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGAGCCTGTTGTCTACAAGTC
                     1270      1280      1290      1300      1310      1320


                     1210      1220      1230      1240      1250      1260
ss.AR350065      TAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCKAACAGAACAAYTGACTGAGGYTAKRG
                 *********************************************  ************* ***
ss.DNA57033      TAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAAC-ACTGACTGAGGCT-TAG
                     1330      1340      1350      1360      1370


                     1270      1280      1290      1300      1310      1320
ss.AR350065      GGGWTGTGACCTCTAGACTKTGGGSTKSCAYTTGCWTGGYTGAGCAACCCTGGGAAAAGT
                 ******************* **************** **********************
ss.DNA57033      GGGATGTGACCTCTAGACTGGGGGGCTGCCACTTGC-TGGCTGAGCAACCCTGGGAAAAGT
                   1380      1390      1400      1410      1420      1430
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ss.AR350065     GACTTCATCCCTTXGGTCCXAAGTTTTCTCATCTGTAATGGGGGA--TXCCTACAAAACT
                ************* ***** *********************** * ****** * **
ss.DNA57033     GACTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACCTACACACCT
                  1440        1450        1460        1470        1480        1490


ss.AR350065     G
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ss.DNA57033     GCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAATACACCC
                  1500        1510        1520        1530        1540        1550

ss.DNA57033     AGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTCAGTGTTT
                  1560        1570        1580        1590        1600        1610

ss.DNA57033     CTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGTGGC
                  1620        1630        1640        1650        1660        1670

ss.DNA57033     TTGGAGAGCCCACTTTCCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGGT
                  1680        1690        1700        1710        1720        1730

ss.DNA57033     GTTGAGTTCACTTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAG
                  1740        1750        1760        1770        1780        1790

ss.DNA57033     TAGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGG
                  1800        1810        1820        1830        1840        1850

ss.DNA57033     ATCCATGAACTACTGTAAAGTGTTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATG
                  1860        1870        1880        1890        1900        1910

ss.DNA57033     TATGTGTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTTGTGCTCC
                  1920        1930        1940        1950        1960        1970

ss.DNA57033     TTTTTTCTGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGC
                  1980        1990        2000        2010        2020        2030

ss.DNA57033     GGTAAAAAAAAAAAAAAAAA
                  2040        2050
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